

REMARKS

Formal Matters

A substitute specification, revised sequence listing and formal drawings are provided in order to correct various errors of form. Responsive to the Examiner's remark concerning the priority information, the paragraph at page 1, line 12 has been appropriately revised.

In amended Figures 1A-1E, Figures 2A-2B, Figures 3A-3D, Figure 4, Figure 5, Figures 6A-6F, Figure 7A-7B, Figures 8A-8D, Figure 9, Figure 10A-10D and Figure 11A-B, extraneous text was removed from the Figures.

Claims 29-54 remain in this application. No claim has been canceled. Claims 29, 39 and 49 are amended. No new matter is added by the amendments.

Support for the amendments to claims 29, 39, 49 is found at least at page 49, lines 33-36.

In view of the Examiner's earlier 6-way restriction requirement in parent application USSN 09/292,505, now U.S.P. 6,348,575, applicant retains the right to present previously withdrawn and cancelled claims in a divisional application.

The Rejection under 35 U.S.C. § 101

Claims 29-34, 37, 39-44, 47, 49-50 and 53 are rejected under 35 U.S.C. § 101 allegedly for being directed to non-statutory subject matter.

In response, Applicants amendment renders the rejection moot.

The Rejection under 35 U.S.C. § 102(e)

Claims 29-35, 37-45, 47-51, and 53-54 are rejected under 35 U.S.C. § 102(e) as allegedly being anticipated by U.S. Patent No. 6,309,879. Specifically, the Examiner has alleged that the above claims are drawn to antibodies which bind to polypeptides that are at least 91%, 92%, 93%, 95% or 100% identical to SEQ ID NO:2. The Examiner further alleges that the '879 patent not only teaches a polypeptide sequence that is 99.6% identical to SEQ ID NO:2, but also antibodies binding to such polypeptide sequence.

In response, Applicants respectfully submit that the 6,309,879 patent was the losing party to Applicants' related application USSN 09/060,939, having the same inventors and filing date as the parent application (USSN 09/292,505, U.S.P. 6,348,575) of the pending application. The U.S.P.T.O. has already determined in a prior action that Applicants are the actual inventors of the subject matter claimed in the '879 patent. A copy of the final decision from Interference 105,081 awarding all of claims 1-13 of '879 patent to Applicant's 09/060,939 application appears in the Appendix.

Applicants respectfully request reconsideration and withdrawal of the rejection of Claims 29-35, 37-45, 47-51, and 53-54 under 35 U.S.C. § 102(e)

The Rejection Under 35 U.S.C. § 103(a) (cited references)

Claims 36, 46, and 52 are rejected under 35 U.S.C. § 103(a) as being allegedly unpatentable over the '879 patent as applied to claims 29-35, 37-45, 47-51, and 53-54 above, and further in view of Berkower.

In response, Applicants response above under the 102 reference has eliminated the relevance of the '879 patent to the pending claims. Berkower does not teach, disclose or infer antibodies that bind SEQ ID NO:2.

Applicants respectfully request reconsideration and withdrawal of the rejection of Claims 36, 46 and 52 under 35 U.S.C. § 103(a).

SUMMARY

Claims 29-54 are pending in the application. Claims 29, 39 and 49 have been amended without prejudice to later prosecution.


If in the opinion of the Examiner, a **telephone conference** would expedite the prosecution of the subject application, the Examiner is **strongly encouraged** to call the undersigned at the number indicated below.

This response/amendment is submitted with a transmittal letter. In the unlikely event that this document is separated from the transmittal letter or if fees are required, applicants petition the Commissioner to authorize charging our Deposit Account 07-0630 for any fees required or credits due and any extensions of time necessary to maintain the pendency of this application.

Applicants respectfully request that a timely Notice of Allowance be issued in this case.

Respectfully submitted,
GENENTECH, INC.

Date: March 21, 2005

By: 

Craig G. Svoboda
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Appendix

Apr-04-2003 11:40

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T-587

P.002/004

F-011

The opinion in support of the decision being
entered today is not binding precedent of the Board.

Paper 13

Filed by: Trial Section Merits Panel
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Filed
4 April 2003

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS
AND INTERFERENCES

DAVID A. BUMCROFT,

Junior Party
(Patent No. 6,309,879),

v.

FREDERIC DE SAUVAGE
and DAVID A. CARPENTER,

Senior Party
(Application No. 09/060,939).

FAXED

APR 4 - 2003

**PAT. & T.M. OFFICE
BOARD OF PATENT APPEALS
AND INTERFERENCES**

Patent Interference 105,081 (NAGUMO)

Before SCHAFER, LANE, and NAGUMO, Administrative Patent Judges.
NAGUMO, Administrative Patent Judge.

JUDGMENT

(Pursuant to 37 CFR § 1.662(a))

Introduction

1. On April 2, 2003, junior party Bumcroft filed Paper 12, in which it conceded priority as to Count 1, the sole count in this interference, and acknowledged that the communication would be treated as a request for adverse judgment.

Apr-04-2003 11:40

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T-557 P.009/004 F-011

Interference 105,081
Bumcrot v. De Sauvage

Paper No. 13

Order


On consideration of the forgoing, it is:

ORDERED that judgment on priority as to Count 1 is awarded
against junior party Bumcrot;

FURTHER ORDERED that Bumcrot is not entitled to a patent
containing claims 1-13 of Bumcrot's 6,309,879 patent, which
correspond to Count 1;

FURTHER ORDERED that copies of this decision be given
appropriate paper numbers and be entered in the administrative
record of Bumcrot's 6,309,879 patent and De Sauvage's 09/060,939
application.


RICHARD E. SCHAFER
Administrative Patent Judge


SALLY GARDNER LANE
Administrative Patent Judge


MARK NAGUMO
Administrative Patent Judge

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INTERFERENCES

INTERFERENCE
TRIAL SECTION

Apr-04-2003 11:41

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T-587 P.004/004 F-011

Paper No. 13

Interference 105,081
Bumcrot v. De Sauvage

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UNITED STATES PATENT AND TRADEMARK OFFICE
TRIAL DIVISION

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Remarks:

If you have not received all copies of this transmission, please contact this Office as soon as possible at: (703)308-8797.

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1/27
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1 GGTATTTCAG GCCATGGTGT TCGCGCGGAAT TAATTCCCGA TCCAGACATG ATAAGATACA TTGATGAGTT TGGACAAACC ACAACTAGAA TGCAGTGA
CAATAAAGTC CGGTACCACA ACGCGGCTTA ATTAAGGGCT AGGTCTGTAC TATTCTATGT AACTACTCAA ACCTGTTTGG TGTGATCTT ACGTCACTTT
101 AAAAATGCTTT ATTTGTGAAA TTTGTGATGC TATTGCTTTA TTTGTAACCA TTATAAGCTG CAATAAACA GTTGGGCCAT GCGGGCCAAAG CTTCTGCAGG
TTTACGAAA TAAACACTTT AAACACTACG ATAACGAAAT AAACATTTGT AATATTGAC GTTATTGTT CAACCCGTA CCGCCGGTTC GAAGACGTCC
201 TCGACTCTAG AGGATCCCG GGAATTCCG GCATGACTCG ATCGCCGCGC CTCAGAGAGC TCGCCCCGAG TTACACACCC CCAGCTCGAA CCGCAGCACCC
AGCTGAGATC TCCTAGGGC CCCTTAAGG CGTACTGAGC TAGCGGCGG GAGTCTCTCG ACGGGGCTC AATGTGTGG GGTGAGCTT GCGTCTGTTG
M T R S P P L R E L P P S Y T P P A R T A A P
3 1 ~~insert starts here~~ (SEQUENCE 2)
301 CCAGATCCTA GCTGGGAGCC TGAAGGCTCC ACTCTGGCTT CGTGCTTACT TCCAGGGCCT GCTCTTCTCT CTGGGATGCG GGATCCAGAG ACATTGTGGC
GGTCTAGGAT CGACCCCTCG ACTTCCGAGG TGAGACCGAA GCACGAATGA AGGTCCCGGA CGAGAAGAGA GACCCCTACG CCTAGGTCTC TGTAACACCG
24 Q I L A G S L K A P L W L R A Y F Q G L L F S L G C G I Q R H C G
401 AAAGTCTCT TTCTGGGACT GTTGGCCTTT GGGGCCCTGG CATTAGTCT CCGCATGGCC ATTATTGAGA CAACTTTGA ACAGCTCTGG GTAGAAAGTGG
TTTACGAGA AAGACCCCTGA CAACCGGAAA CCGCGGAGC GTAATCCAGA GCGGTACCGG TAATAACTCT GTTTGAACCT TGTCGAGACC CATCTTCACC
57 K V L F L G L L A F G A L A L G L R M A I I E T N L E Q L W V E V G
501 GCAGCCGGGT GAGCCAGGAG CTCGATTACA CCAAGGAGAA GCTGGGGAG GAGCTGCAT ACACCTCTCA GATGCTGATA CAGACCGCAC GCCAGGAGGG
CGTCGGCCCA CTCGGTCTC GACGTAATGT GTTCTCTCTT CGACCCCTC CTCCGACGTA TGTGGAGAGT CTACGACTAT GTCTGGCGTG CCGTCTCTCC
91 S R V S Q E L H Y T K E K L G E A A Y T S Q M L I Q T A R Q E G
601 AGAGAACATC CTCACACCCG AAGCACTTGG CCTCCACCTC CAGGCAGCCC TCACTGCCAG TAAAGTCCAA GTATCACTCT ATGGGAAGTC CTGGGATTG
TCTCTTTAG GAGTGTGGC TTCGTGAACC GGAGGTGGAG GTCCGTCCGG AGTGACGTC ATTCAGGTT CATAGTGAGA TACCCTTCAG GACCCTAAC
124 E N I L T P E A L G L H L Q A A L T A S K V Q V S L Y G K S W D L
701 AACAAATCT GCTACAAATC AGGAGTTCCC CTTATTGAAA ATGGAATGAT TGAGTGGATG ATTGAGAAGC TGTTCCTGTG CGTGATCCTC ACCCCCTCG
TTGTTTGA GAATGAGG TCCTCAAGG GAATAACTTT TACCTTACTA ACTCACTAC TAACCTCTTCG ACAAGGCAC GCACCTAGGAG TGGGGGAGC
157 N K I C Y K S G V P L I E N G M I E W M I E K L F P C V I L T P L D
801 ACTGCTTCTG GGAGGAGCC AAACCTCCAG GGGCTCCG CTACCTGCC GCGCGCCCGG ATATCCAGTG GACCAACCTG GATCCAGAGC AGCTGCTGGA
TGACGAAGAC CCTCCCTCGG TTTGAGGTTT CCGGAGGCG GATGAGCGG CATAGGTCAC CTGCTGAGC CTAGGTCTCG TCGACGACCT
191 C F W E G A K L Q G G S A Y L P G R P D I Q W T N L D P E Q L L E

FIG. 1A

901 GGAGCTGGGT CCCTTTGCCT CCTTGAGGG CTTCGGGAG CTGTAGACA AGGCACAGGT GGGCCAGGC TACGTGGGC GGCCTGTCT GCACCTGAT
 CCTCGACCA GGAACCGA GGAACCTCC GAAGCCCTC GACGATCTGT TCCGTGTCCA CCGGTCCG ATGCACCCG CCGGACAGA CGTGGGACTA
 224 E L G P F A S L E G F R E L L D K A Q V G Q A Y V G R P C L H P D
 1001 GACCTCCACT GCCCACCTAG TGCCCCAAC CATCACAGCA GCGAGGCTC CAATGTGGCT CACGAGCTGA GTGGGGGCTG CCATGGCTTC TCCACAAA
 CTGAGGTGA CCGGTGATC ACGGGGTG GTAGTGTCT CCGTCCGAG GTTACACCGA GTGCTCGACT CACCCCGGAC GGTACCGAAG AGGTGTTTA
 257 D L H C P P S A P N H H S R Q A P N V A H E L S G G C H G F S H K F
 1101 TCATGCACTG GCAGGAGAA TTGCTGCTGG GAGGCATGG CAGAGACCC CAGAGAGAGC TGCTGAGGC AGAGGCCCTG CAGAGCACCT TCTTGCTGAT
 AGTACGTGAC CGTCTCTCTT AACGACGACC CTCGCTACCG GTCTCTGGG GTTCTCTCTG ACCTCTCCG TCTCCGGGAC GTCTCGTGA AGAAGACTA
 291 M H W Q E E L L L G G M A R D P Q G E L L R A E A L Q S T F L L M
 1201 GAGTCCCCGC CAGCTGTACG AGCATTTCCG GGGTGACTAT CAGACACATG ACATTGGCTG GAGTGAGGAG CAGGCCAGCA CAGTGCTACA AGCCTGGCAG
 CTCAGGGCG GTGACATGC TCGTAAAGC CCCACTGATA GTCTGTGTAC TGTAAACGAC CTCACTCTC GTCCGTCGT GTCCGTCGT GTCACGATGT TCGGACCGTC
 324 S P R Q L Y E H F R G D Y Q T H D I G W S E E Q A S T V L Q A W Q
 1301 CGCGCTTTG TGACGTGGC CCAGGAGGC CTGCTTGAGA ACGTTTCCA GCAGATCCAT GCCTTCTCCT CCACACCCCT GGATGACATC CTGCATGCGT
 GCGCGAAGC ACGTCGACCG GGTCTTCCG GACGACTCT TCGAAGGGT CGTCTAGTA CGGAAGAGGA GTTGGTGGG CCTACTGTAG GACTACGCA
 357 R F V Q L A Q E A L P E N A S Q Q I H A F S S T T L D D I L H A F
 1401 TCTGTGAAGT CAGTGTGCTCC CGTGTGGTG GAGGTATCT GCTCATGCTG GCCTATGCCT GTGTGACCAT GCTGCGGTG GACTGCGCC AGTCCAGGG
 AGAGACTTCA GTCACGACCG GCACACCCACC CTCGATAGA CGAGTACGAC CGGATACCGA CACACTGGTA CGACGCCACC CTGACGCGGG TCAGGTGCCC
 391 S E V S A A R V V G G Y L L M L A Y A C V T M L R W D C A Q S Q G
 1501 TTCCCTGGGC CTGCGCGGG TACTGTGCT GGCCTGGCG GTGGCCTCAG GCCTTGGGCT CTGTGCCCTG CTCGGCATCA CCTTCAATGC TGCCACTACC
 AAGGACCCG GAACGGCCCC ATGACGACCA CCGGGACCG CACCGGAGT CCGAACCCGA GACACGGGAC GAGCCGTAGT GGAAGTTACG ACGGTGATGG
 424 S V G L A G V L L V A L A V A S G L G L C A L L G I T F N A A T T
 1601 CAGGTGCTGC CTTTCTTGGC TCTGGGAATC GCGGTGGATG ACGTATTCTC GCTGGCGCAT GCCTTCACAG AGGCTCTGCC TGGCACCCCT CTCCAGGAGC
 GTCCACACG GAAAGAACG AGACCTTAG CCGCACCTAC TGCATAAGGA CGACCGCGTA CGGAAGTGT TCCGAGACGG ACCGTGGGGA GAGGTCTCTC
 457 Q V L P F L A L G I G V D D V F L L A H A F T E A L P G T P L Q E R
 1701 GCATGGGCGA GTGTCTGCAG CCGACGGGCA CCAGTGTGCT ACTCACATCC ATCAACAACA TGGCGGCTT CCTCATGGCT GCCCTCGTTC CCATCCCTGC
 CGTACCCCT CACAGACGTC GCGTCCCGT GTTCACAGCA TGAGTGTAGG TAGTGTGTGT ACCGGGGA A GAGTACCGA CCGGAGCAAG GGTAGGGACG
 491 M G E C L Q R T G T S I N N M A A F L M A A L V P I P A

FIG. 1B

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1801 GCTGCGAGCC TTCTCCCTAC AGCGGGCCAT AGTGGTTGGC TGACACCTTTG TAGCCGTGAT GCTTGCTTTC CCAGCCATCC TCAGCCTGGA CCTACGGCGG
 CGACGCTCGG AAGAGGGATG TCCGCCGGTA TCACCAACCG ACGTGGAAC ATCGGCACTA CGAACAGAAG GGTGCGTAGG AGTCGGACCT GGATGCCGCC
 524 L R A F S L Q A A I V V G C T F V A V M L V F P A I L S L D L R R
 1901 CGCCACTGCC AGCGCCTTGA TGTCTCTGTC TGCTCTCTCA GTCCCTGCTC TGCTCAGGTG ATTCAGATCC TGCCCCAGGA GCTGGGGGAC GGGACAGTAC
 GCGGTACCG TCGCGGAAT ACACGAGACG ACGAAGAGGT CAGGGACGAG ACGAGTCCAC TAAGTCTAGG ACGGGTCTCT CGACCCCTG CCCTGTCTATG
 557 R H C Q R L D V L C C F S S P C S A Q V I Q I L P Q E L G D G T V P
 2001 CAGTGGGCAT TGCCACCTC ACTGCCACAG TTCAAGCCTT TACCACCTGT GAAGCCAGCA GCCAGCATGT GGTCAACATC CTGCCCTCCC AAGCCCACCT
 GTCACCCGTA ACGGGTGGAG TGACGGGTGTC AAGTTCGGAA ATGGGTGACA CTTCGGTCTG CCGTCTGTACA CCAGTGGTAG GACGGAGGGG TTCGGGTGGA
 591 V G I A H L T A T V Q A F T H C E A S S Q H V V T I L P P Q A H L
 2101 GGTGCCCTCA CCTTCTGACC CACTGGGCTC TGAGCTCTTC AGCCTGGAG GGTCCACACG GGACCTTCTA GGCAGGAGG AGGAGACAAG GCAGAAGGCA
 CCACGGGGGT GGAAGACTGG GTGACCCGAG ACTCGAGAAG TCGGACCTC CCAGGTGTGC CCGTGAAGAT CCGTCTCTCC TCCTCTGTTT CCGTCTCTCCG
 624 V P P P S D P L G S E L F S P G G S T R D L L G Q E E T R Q K A
 2201 GCCTGCAAGT CCCTGCCCTG TGCCCGCTGG AATCTTGCCC ATTTGCGCCG CTATCAGTTT GCCCGGTTGC TGCTCAGTC ACATGCCAAG GCCATCGTGC
 CGGACGTTCA GGCACGGGAC ACGGCGGACC TTAGAACGGG TAAAGCGGC GATAGTCAA CCGGGCAACG ACGAGGTACG TGTACGGTTC CCGTAGCACG
 657 A C K S L P C A R W N L A H F A R Y Q F A P L L L Q S H A K A I V L
 2301 TGGTGCTCTT TGGTGCTCTT CTGGGCCCTGA GCCTCTACGG AGCCACCTTG GTGCAAGACG GCCTGGCCCT GACGGATGTG GTGCCTCGG GCACCAAGGA
 ACCACGAGAA ACCACGAGAA ACCACGAGAA GACCCGGACT CCGAGATGCC TCGGTGGAAC CAGCTTCTGC CCGACCGGGA CTGCCCTACAC CACGGAGCCC CCGTGTCTCT
 691 V L F G A L L G L S L Y G A T L V Q D G L A L T D V V P R G T K E
 2401 GCATGCCCTC CTGAGCGCCC AGCTCAGGTA CTTCTCCCTG TACGAGGTGG CCCTGGTGAC CCAGGTGGC TTGACTACG CCATTTCCCA ACGCGCCCTC
 CGTACGGGAG GACTCGCGGG TCCAGTCCAT GAAGAGGGAC ATGCTCCACC GGGACCACTG GGTCCACCG GGTGATGC AAAGTATGC GGTAAAGGT TCGCGGGGAG
 724 H A F L S A Q L R Y F S L Y E V A L V T Q G G F D Y A H S Q R A L
 2501 TTTGATCTGC ACCAGCGCTT CAGTTCCCTC AAGCGGTGTC TGCCCCCACC GGCACCCAG GCACCCCGCA CCTGGCTGCA CTATTACCG AACTGGCTAC
 AAAGTAGACG TGGTCCGCA GTCAAGGGAG TTCCGCCACG ACGGGGTGG CCGGTGGGT CCGTGGGGGT GGACCGACGT GATAATGGCG TTGACCGATG
 757 F D L H Q R F S S L K A V L P P P A T Q A P R T W L H Y Y R N W L Q
 2601 AGGGAATCCA GGCTGCCCTT GACCAGGACT GGGCTTCTGG GGCATCACC CGCCTCTCT ACCGCAATGG CTCTGAGGAT GGGGCCCTCG CCTACAAGCT
 TCCCTTAGGT CCGACGGAAA CTGGTCTGA CCCGAAGACC CCGGTAGTGG GCGGTAGCA TGGCGTTACC GAGACTCCTA CCGCGGGACC GGATGTTCTGA
 791 G I Q A A F D Q D W A S G R I T R H S Y R N G S E D G A L A Y K L

FIG. 1C

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2701 GCTCATCCAG ACTGGAGACC CCCAGGAGCC TCTGGATTTT AGCCAGCTGA CCACAAGGAA GCTGGTGGAC AGAGAGGGAC TGATTCCACC CGAGCTCTTC
CGAGTAGGTC TGA~~CCT~~CTGC GGGTCCCTCG AGACCTAAAG TCGGTCCACT GGTGTTCTT CGACCACCTG TCTCTCCCTG ACTAAGGTGG GCTCGAGAAG
924 L I Q T G D A Q E P L D F S Q L T T R K L V D R E G L I P P E L F
2801 TACATGGGC TGACCTGTG GGTGAGCAGT GACCCCTGG GTCTGGCAGC CTCACAGGCC AACTTCTACC CCCACCTCC TGAATGGGTG CACGACAAAT
ATGTA~~CCCC~~CG ACTGGACAC CCACTCGTCA CTGGGGGACC CAGACCGTCG GAGTGTCCGG TTGAAGATGG GGGGTGGAGG ACTTACCGAC GTGCTGTTTA
857 Y M G L T V W V S S D P L G L A A S Q A N F Y P P P P E W L H D K Y
2901 ACGACACCAC GGGGAGAAC CTTCGCATCC CGCCAGCTCA GCCCTTGGAG TTTGCCCACT TCCCTTCTT GCTGCGTGGC CTCCAGAAGA CTGCAGACTT
TGCTGTGGTG CCCCCTCTTG GAAGCGTAGG GCGGTCCAGT CGGGAACCTC AAACGGGTCA AGGGGAAGGA CGACGCACCG GAGGTCTTCT GACGTCTGAA
891 D T T G E N L R I P P A Q P L E F A Q F P F L L R G L Q K T A D F
3001 TGTGGAGCC ATCGAGGGG CCCGGGCAGC ATGGCGCAGG GCCGGCCAGG CTGGGGTGCA CGCTACCCC AGCGGTCCC CTTCTCTCTT CTGGGAACAG
ACACCTCCG TAGCTCCCC GGGCCCGTCG TACCGTCTC CGGCCGGTCC GACCCACAGT CGGATGGG TCGCCGAGG GGAAGGAGAA GACCTTGTG
924 V E A I E G A R A A C A E A G Q A G V H A Y P S G S P F L F W E Q
3101 TATCTGGGC TCGGGCGCTG CTTCCTGCTG GCCGTCTGCA TCCTGTGGT GTGCACTTTC CTCTGCTGTG CTCTGCTGCT CCTCAACCCC TGGACGGCTG
ATAGACCCG ACGCCGCGAC GAAGGACGAC CGGCAGACGT AGGACGACCA CACGTGAAG GAGCAGACAC GAGACGACGA GGAGTTGGG ACCTGCCGAC
957 Y L G L R R C F L L A V C I L L V C T F L V C A L L L L N P W T A G
3201 GCCTCATAGT GCTGGTCTG GCGATGATGA CAGTGGAAT CTTTGGTATC ATGGGTTTC TGGGCATCA GCTGAGTGCC ATCCCCGTGG TGATCCTTGT
CGGAGTATCA CGACCAGGAC CGCTACTACT GTCACTTGA GAAACCATAG TACCCAAAGG ACCCGTAGTT CGACTCACGG TAGGGGCACC ACTAGGAACA
991 L I V L V L A M M T V E L F G I M G F L G I K L S A I P V V I L V
3301 GGCTCTCTGA GGCATTGGCG TTGAGTTTCA AGTCCACGTG GCTCTGGCT TCCTGACCAC CCAGGGCAGC CGGAACCTGC GGGCCGCCCA TGCCCTTGAG
CCGGAGACAT CCGTAACCGC AACTCAAGT TCAGGTGCAC CGAGACCCGA AGGACTGGTG GGTCCCGTCG GCCTTGGACG CCCGGCGGT ACGGAACATC
1024 A S V G I G V E F T V H V A L G F L T T Q G S R N L R A A H A L E
3401 CACACATTG CCCCCTGAC CGATGGGGC ATCTCCACAT TGCTGGGTCT GCTCATGCTT GCTGTTTCCC ACTTTGACTT CATTTGAAG TACTTCTTTG
GTGTGTAAC GGGGCACTG GCTACCCCGG TAGAGGTGTA ACGACCCAGA CGAGTACGAA CGACCAAGG TGA~~AACT~~GAA GTAACATTCC ATGAAGAAC
1057 H T F A P V T D G A I S T L L G L L M L A G S H F D F I V R Y F F A
3501 CGCGCTGAC AGTGCTCAG CTCCTGGGC TCCTCCATGG ACTCGTGTG CTGCCTGTG TGCTGTCCAT CCTGGGCCG CCGCCAGAGG TGATACAGAT
GCGCGACTG TCACGAGTGC GAGGACCCG AGGAGGTACC TGAGCACGAC GACGGACACG ACGACAGGTA GGACCCGGC GCGGTCTCC ACTATGTCTA
1091 A L T V L T L L G L L H G L V L L P V L L S I L G P P P E V I Q M

FIG. 1D

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3501 GTACAAGGAA AGCCACAGAGA TCCTGAGTCC ACCAGCTCCA CAGGAGGCG GGCTTAGGTG GGGGGCATCC TCCTCCCTGC CCCAGAGCTT TGCCAGAGTG
CATGTTCCCTT TCGGGTCTCT AGGACTCAGG TGGTCGAGGT GTCCCTCCGC CCGAATCCAC CCCCCTAGG AGGAGGACG GGGTCTCGAA ACGTCTCACC
1124 Y K E S P E I L S P P A P Q G G G L R W G A S S S L P Q S F A R V
3701 ACTACCTCCA TGACCGTGGC CATCCACCCA CCCCCCTGC CTGGTGCTA CATCCATCCA GCCCCTGATG AGCCCCCTTG GTCCCCCTGCT GCCACTAGCT
TGATGAGGT ACTGGCACCG GTAGGTGGGT GGGGGGACG GACCACGGAT GTAGGTAGGT CGGGGACTAC TCGGGGAAAC CAGGGGACGA CGGTGATCGA
1157 T T S M T V A I H P P P L P G A Y I H P A P D E P P W S P A A T S S
3801 CTGGCACTT CAGTTCCAGG GGACCAAGGC AGCTGAAGCA CAGACACCAT GTGTGGGCG TGTGGGTCA CTGGGAAGCA
GACCGTTGGA GTCAAGGTCC CCGGTCCAG GTCGGTGACC CACTTCTCG TCGACTTCGT GTCTCTGGTA CACACCCCGC ACACCCACGT GACCCCTTCGT
1191 G N L S S R G P G P A T G O
3901 CTGGGTCTGG TGTTAGACGC AGGACGGACC CCTGGAGGC CTGCTGCTG CTGCATCCCC TCTCCGACC CAGCTGTCTAT GGGCCTCCCT GATATCGAAT
GACCCAGACC ACAATCTGCG TCCTGCCCTGG GGACCTCCCG GGACGACGAC GACGTAGGGG AGAGGGCTGG GTCGACAGTA CCGGAGGGA CTATAGCTTA
~~PRK follows, this is the 5' prime end of vector~~
~~up to C (silent)~~
4001 TCAATCGATA GAACCGAGGT GCAGTTGGAC
ACTTAGCTAT CTGGCTCCA CGTCAACCTG

FIG. 1E

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(SEQ ID NO: 3)
          30          40          50          60          70
905531    GCTGGGGTGCACGCCTACCCNAGCGGNTCCCCCTTCCTCTTCTGGGAACA
          ::: :: : *****
hpatched  CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA
(SEQ ID NO: 4)
          3010         3020         3030         3040         3050

          80          90          100         110          120
905531    GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
          *** * *****
hpatched  GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTTCATCAGCGTGGTGTGG
          3060         3070         3080         3090         3100

          130         140         150         160         170
905531    TGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTNAACCCCTGGACGGCT
          *****
hpatched  CCTGCACATTTCCTCGTGTGCGCTGTCTTCCTTCTGAACCCCTGGACGGCC
          3110         3120         3130         3140         3150

          180         190         200         210         220
905531    GGCTNATAGTGCTGGTCCTGGCGATGATGACAGTGGAACCTTTGGTAT
          ** *****
hpatched  GGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTCCGGCAT
          3160         3170         3180         3190         3200

          230         240         250
905531    CATGGGTTTNCCTGGGCATCAAGCTGAGT
          *****
hpatched  GATGGGCCTCATCGGAATCAAGCTCAGT
          3210         3220         3230

          80          90          100         110          120
905531    TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
          ::: :: : *****
hpatched  GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC---TGCACATTTCCTCGTGT
          3090         3100         3110         3120

          130         140         150
905531    GCACTTTCCTCGTCTGTGCTCTGCTGCT
          ** * * * *
hpatched  GCGCTGTCTTCCTTCTGAACCCCTGGAC
          3130         3140         3150

```

FIG. 2A

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(SEQ ID NO. 5) 1326258 30 40 50 60 70
 GCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACA
 : : : : * * * * *
 hpatched CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA
 3010 3020 3030 3040 3050

1326258 80 90 100 110 120
 GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
 * * * * *
 hpatched GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTTCATCAGCGTGGTGTGG
 3060 3070 3080 3090 3100

1326258 130 140 150
 TGTGCACTTTCCTCNTCTGTGCTCT
 * * * * *
 hpatched CCTGCACATTCCTCGTGTGCGCTGT
 3110 3120 3130

1326258 90 100 110 120 130
 TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
 : : : * * * * *
 hpatched GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC---TGCACATTCCTCGTGT
 3090 3100 3110 3120

1326258 140 150
 GCACTTTCCTCNTCTGTGCTCT
 * * * * *
 hpatched GCGCTGTCTTCCTTCTGAACCC
 3130 3140

1326258 10 20 30 40 50
 CCGGGCAGCATGCGCAGAGGCCCGCCAGGCTGGGGTGCACGCCTACCCCA
 * * * * *
 (SEQ ID NO. 6) hpatched.RC CCGGGCGGCATG--GCGAAGCGGACCGCTGGGGGCTGGCTCAGGGGAG
 710 720 730 740 750

FIG. 2B

~~(SEQ ID NO: 4)~~
~~(SEQ ID NO: 2)~~

1 MASAGNAAEPODRGGGGSGCIGAPRPAAGGRRRTGGLRRAAA[PDR]DYL
1MTRSP[PL]REL.
PTCH
PTCH2
51 HRPSYCDAAF[AL]EQISKGKA[TA]GRKAPLWLR[KFQ]RLLF[KL]GCY[IQ]KNC[GK]
11 .PSYTPP[.A]RTAAPQILA[AGSL]KAPLWLR[YFQ]GLLF[SL]GCG[IO]RHCGK
PTCH
PTCH2
101 FLVVG[LL]IFGA[FA]VGLK[AN]LETNVEELWVEVGGRVSRRELNYTRQKIGEE
58 VLLFLG[LL]AFGA[LA]LGLRMA[II]ETNLEQLWVEVGSRVSQELHYTKELGEE
TM1
PTCH
PTCH2
151 AMFNPQLMIOTTPKEEGANVLTTEALQHLDSALQASRVHVMYNRQWKLE
108 AAYTSQMLIOTAROEENILTPREALGLHLQAALTASKVQVSLYGKSWDLN
PTCH
PTCH2
201 HLCYKSGELITE[TE]GYMDQI[IE]YLYPCL[II]TPLDCFWEGAKLQSGTAYL LG
158 KLCYKSGVPLIE[ENG]MIEWMIEK[LFP]CVILTPDCFWEGAKLQSGSAYLPG
PTCH
PTCH2
251 KPPLRWTFDPL[EF]LEELKKINYQVDSWE[EM]LNKAEVGHGYMDRPPCLNPA
208 RPDIQWTNLDPEQLLEELGPFA.SLEGFREL[LD]KAOVGOAYVGRPPCLHPD
PTCH
PTCH2
301 DPDCPATAPNKN[ST]KPLDMA[LV]LNGGCHGLSRKYMHWQEELIVGGTVKNS
257 DLHCPPSA[PN]HHSRQAPNV[AHE]LSGGCHGFS[HK]FMHWQEELLLGGMARDP
PTCH
PTCH2
351 TGKLVSAHALQ[TM]FQL[MT]PKQ[CM]YEHFKGYEYVSH[.T]NWNEDKAAAIL EAW
307 QGELLRAEALQSTFLLMS[PR]QLYEHRG.DYQTHDILGWSEEQASTVLQAW
TM2
PTCH
PTCH2
400 QRTYVEV[VH]OSV[AN]STQKVLS[FT]TTTLDLILKSFSDVSVIRVASGYLLM
356 QR[RFV]QLAQEALPENASQ[QI]HAFSSITLDDILHAFSEVSAABVVGCVLLM

FIG. 3A

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PTCH 450 L A Y A C L I T M L R W D C S K S Q G A V G L A G V L L V A L S V A A G L G L C S L I G I S F N A A T
PTCH2 406 L A Y A C V I T M L R W D C A Q S Q G S V G L A G V L L V A L A V A S G L G L C A L L G I T F N A A T

TM3

PTCH 500 T Q V L P F L A L G I G V D D V F L L A H A F S E T G Q N K R I P F E D R T G E C L K R T G A S V A
PTCH2 456 T Q V L P F L A L G I G V D D V F L L A H A F T E A L P G . . T P L Q E R M G E C L Q R T G T S V V

TM4

PTCH 550 L T S I S N V T A F M A A L I P I P A L R A F S L Q A A V V V V E N F A M V L L F P A I L S M D
PTCH2 504 L T S I N N M A A E L M A A L V P I P A L R A F S L Q A A I V V G C T E V A V M L V F P A I L S L D

TM6

TM5

PTCH 600 L Y R R E D R R L D I F C C F T S P C V S R V I Q V E P Q A Y T D T H D N T R Y S P P P P Y S S H S
PTCH2 554 L R R R H C Q R L D V L C C F S S P C S A Q V I Q I L P Q E L G D G T V P V G

PTCH 650 F A H E T Q I T M Q S T V Q L R T E Y D P H T H V Y Y T A E P R S E I S V Q P V T V T Q D T L S C
PTCH2 593 I A H L T A T V Q A F T H C E A S S Q H V V T I L P P Q A H L V P P P S D P L G S

PTCH 700 Q S P E S T S S T R D L L S Q F S D S S L H . . C L E P P C T K W T L S S F A E K H Y A P F L L K P
PTCH2 634 E L F S P G G S T R D L L G Q E E E T R Q K A A C K S L P C A R W N L A H F A R Y Q F A P L L L Q S

TM7

PTCH 748 K A K V V V I F L F L G L L G V S L Y G T T R V R D G L D L T D I V P R E T R E Y D F I A Q F K Y
PTCH2 684 H A K A I V L V L F G A L L L G L S L Y G A T L V Q D G L A L T D V V P R G T K E H A F L S A Q L R Y

PTCH 798 F S F Y N M Y I V T Q K A . D Y P N I Q H L L Y D L H R S F S N V K Y V M L E E N K Q L P K M W L H
PTCH2 734 F S L Y E V A L V T Q G G F D Y A H S Q R A L F D L H O R F S S L K A V L P P P A T Q A P R T W L H

FIG. 3B

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PTCH 847 YFRDWLOG LQDAFDSWETGKIMPNNYKNGSDDGVLAYKLLVQTGSRDKP
PTCH2 784 YYRNWLOG IQAAFDQWASGRITRHSYRNGSEDDGALAYKLLIQTGDAQEP

PTCH 897 IDISQLTKORLVDADGITNPSAFYIYLTAWVSNDPVAYAASQANIRPHRP
PTCH2 834 LDIFSQLTTRKLVLDREGLIPPELFYMGTLVWVSSDPLGLAASQANFYPPPP

PTCH 947 EWHDXADYMPETRLRIPAAEP I EYAOFPFYLNGLRDTSDFFVEAIEKVRT
PTCH2 884 EWLHDXVD.TTGENLRIPPAQPLEFAQFPFLLRGLQKITADFFVEAIEGARA

TM8

PTCH 997 IC SNYTSLG LSSYPNGY PFLFWEQY IGLRHWLLFISVVLACTFLVCAVF
PTCH2 933 AC AEAQAQVHAYPSGSPFLFWEQYLGRLRCFLLAVCILLVCTFLVCA LL

TM9

PTCH 1047 LNPWTAGIIVMVLALMTVELFPGMMGLIGIKLSAVPVVILIASVGIGVEF
PTCH2 983 LNPWTAGLVLVLAMMTVELEFGIMGFLGIKLSAIPVVILVASVGIGVEF

TM10

PTCH 1097 TVHVALAFLTAIGDKNRRRAVLALEHMFAPVLDGAVSTLLGVLMLAGSEFD
PTCH2 1033 TVHVALGFLTITQGSRNLRRAHALEHTTFAPVTDGASTLLGLMLAGSHFD

TM11

PTCH 1147 FIVRYFFA VLAILTILGVNLGLVLLPVLLSFFGPYPPEVSPANGLNRLPTP
PTCH2 1083 FIVRYFFAALT VLTLLGLLHGLVLLPVLLSLLGPPEV IQMYKESPEILS

TM12

PTCH 1197 SPEPPPSVVRFAMPPPGHTHSGSDSSDSEYSSOTTVSGLSEELRHYEAQQG
PTCH2 1133 PPAPOGGGLRWGASSSLPQS.FARVTTMTVAIHPPPLPGAYIHPAPDEP

FIG. 3C

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PTCH 1247 AGG PAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPG
PTCH2 1182 PWS PATSSGNLSSRGPGPATG
PTCH 1297 RQGQPRRDPPREGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARS
PTCH 1347 HNPRNPASTAMGSSVPGYCQPIITVTASASVTVAVHPPPVPGGRNPRGG
PTCH 1397 LCPGYPETDHGLFEDPHVFFHVRCERRDSKVEVIELQDVECEEPRGSSS
PTCH 1447 N

FIG. 3D

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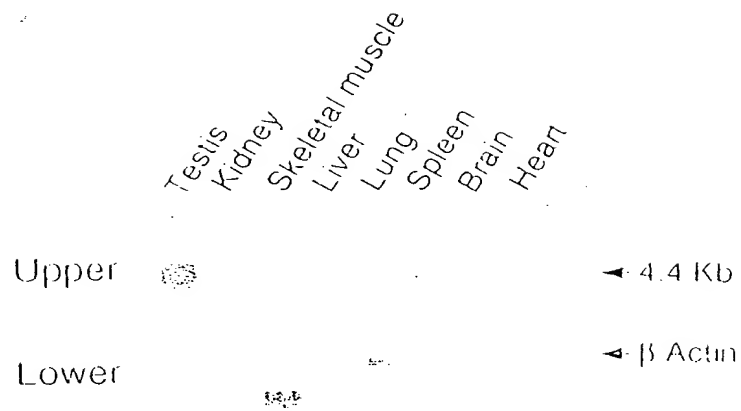


FIG. 4

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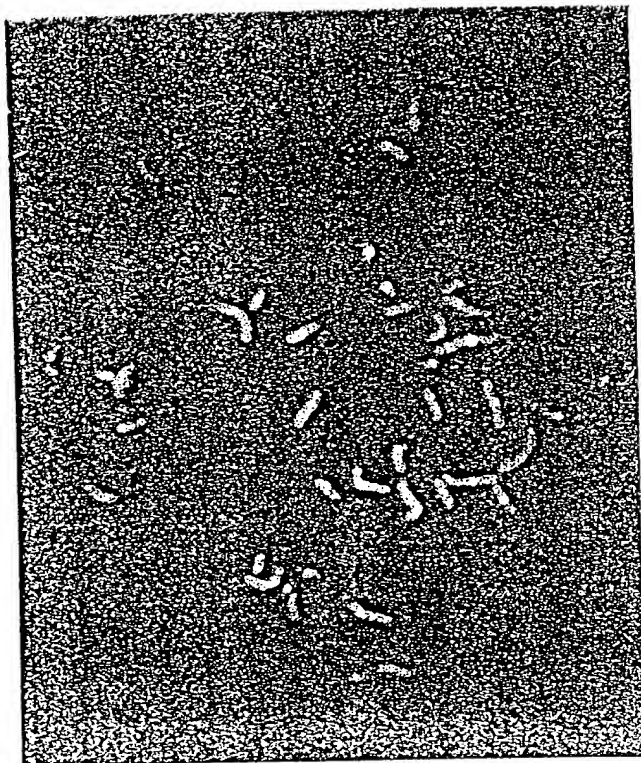


FIG. 5

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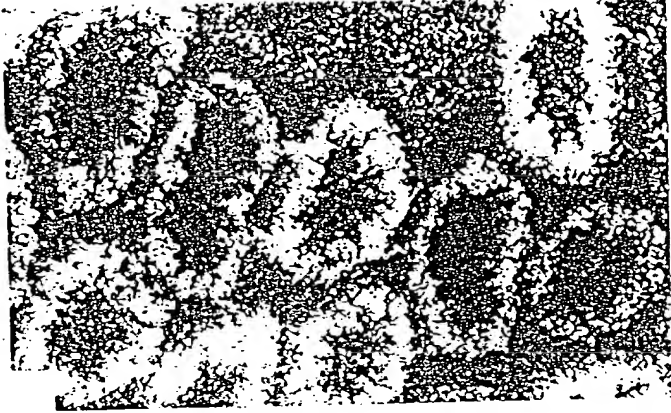


FIG. 6C

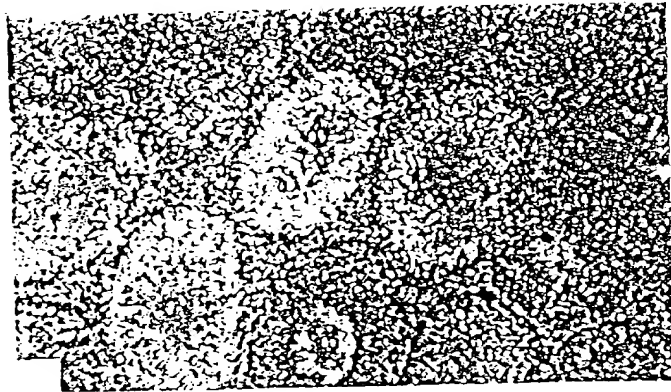


FIG. 6B



FIG. 6A

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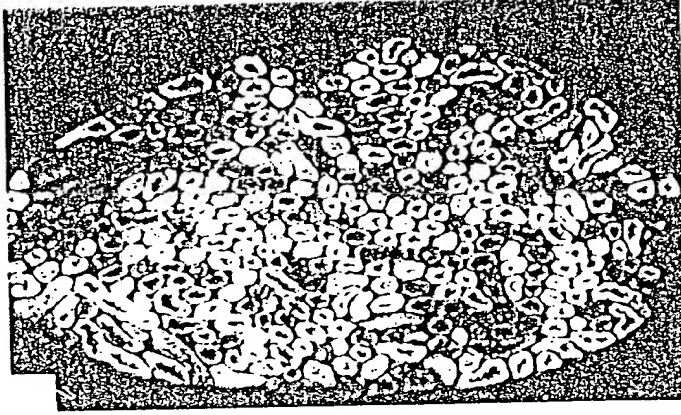


FIG. 6F

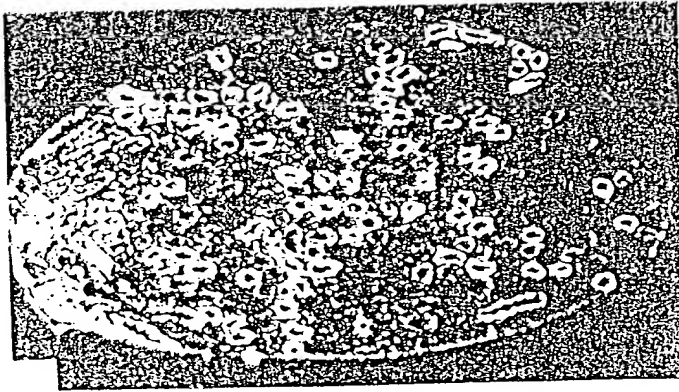


FIG. 6E

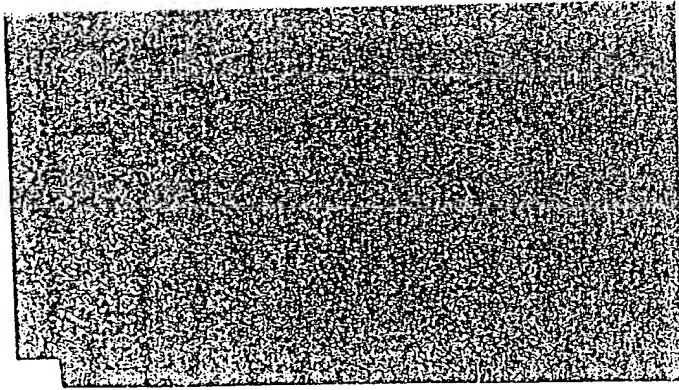


FIG. 6D

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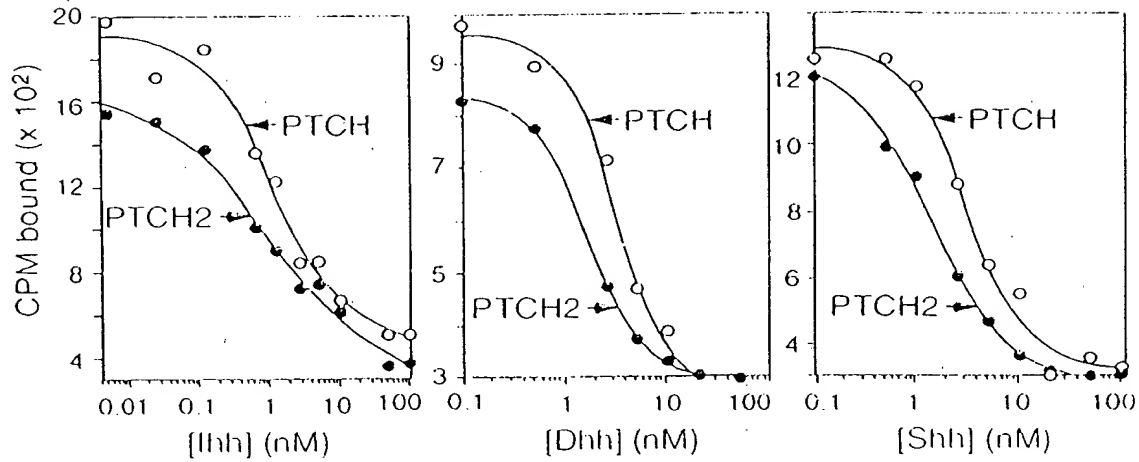


FIG. 7A

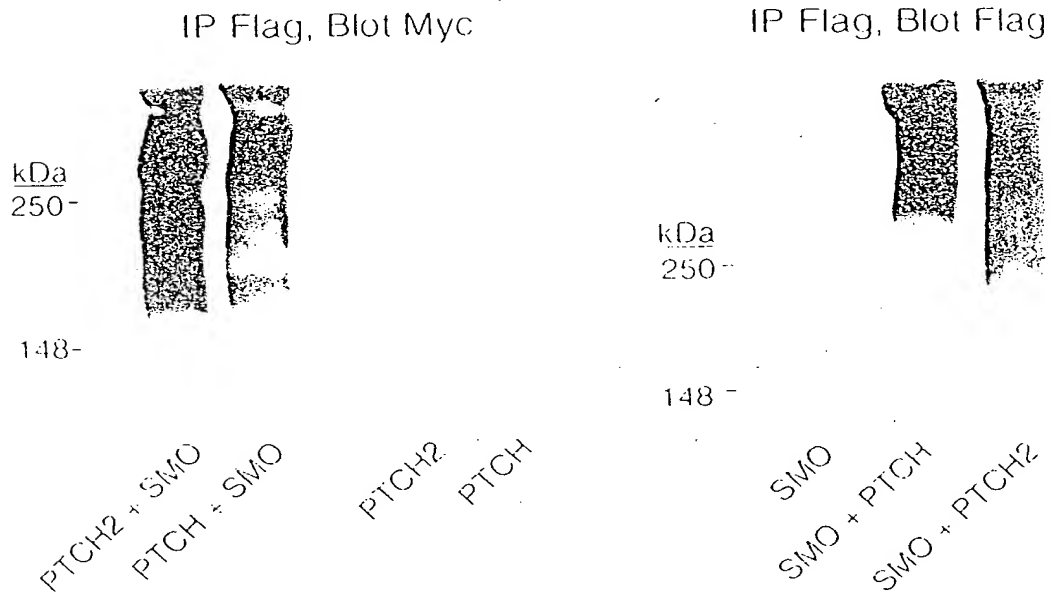


FIG. 7B

	10	20	30	40	50
h <i>Ptch-2</i>	MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCG				
mPatched2	MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCR				
(SEQ ID NO.7)	10	20	30	40	50
	60	70	80	90	100
h <i>Ptch-2</i>	IQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYT				
mPatched2	IQKHCGKVLFLGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYT				
	60	70	80	90	100
	110	120	130	140	150
h <i>Ptch-2</i>	KEKLGEAAAYTSQMLIQATARQEGENILTPEALGLHLQAALTASKVQVSLY				
mPatched2	KEKLGEAAAYTSQMLIQTAHQEGGNVLTPEALDLHLQAALTASKVQVSLY				
	110	120	130	140	150
	160	170	180	190	200
h <i>Ptch-2</i>	GKSVDLNKICYKSGVPLIENGMI EWMI EKLFPCVIL TPLDCFWEGAKLQG				
mPatched2	GKSVDLNKICYKSGVPLIENGM IERMIEKLFPCVIL TPLDCFWEGAKLQG				
	160	170	180	190	200
	210	220	230	240	250
h <i>Ptch-2</i>	GSAYLPGRPD IQWTNLDP EQLLEELGP FASLEG FRELLDKAQVG QAYVGR				
mPatched2	GSAYLPGRPD IQWTNLDP QQLLEELGP FASLEG FRELLDKAQVG QAYVGR				
	210	220	230	240	250
	260	270	280	290	300
h <i>Ptch-2</i>	PCLHPDDLHC PPSAPNHHS RQAPNV AHEL SGGCHGF SHKFMHWQEELL LG				
mPatched2	PCLDPDDPHC PPSAPNRHS RQAPNV AQELS GGCHGF SHKFMHWQEELL LG				
	260	270	280	290	300
	310	320	330	340	350
h <i>Ptch-2</i>	GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQAST				
mPatched2	GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASM				
	310	320	330	340	350

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	360	370	380	390	400
<i>hPtch-2</i>	VLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVG				

<i>mPatched2</i>	VLQAWQRRFVQLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVG				
	360	370	380	390	400
<i>hPtch-2</i>	410	420	430	440	450
	GYLLMLAYACVTMLRWDCAQSQSGVGLAGVLLVALAVASGLGLCALLGIT				

<i>mPatched2</i>	GYLLMLAYACVTMLRWDCAQSGAVGLAGVLLVALAVASGLGLCALLGIT				
	410	420	430	440	450
<i>hPtch-2</i>	460	470	480	490	500
	FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGT				

<i>mPatched2</i>	FNAATTQVLPFLALGIGVDDIFLLAHAFKAPDTPPERMGECLRSTGT				
	460	470	480	490	500
<i>hPtch-2</i>	510	520	530	540	550
	SVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAIL				
	** ** *				
<i>mPatched2</i>	SVALTSVNNMVAFMAALVPIPALRAFSLQAAIVVGCNFAAVMLVFPAIL				
	510	520	530	540	550
<i>hPtch-2</i>	560	570	580	590	600
	SLDLRRRHCRQLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV				

<i>mPatched2</i>	SLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV				
	560	570	580	590	600
<i>hPtch-2</i>	610	620	630	640	650
	QAFTHCEASSQHVVITILPPQAHLVPPSPDPLGSELFSPGGSTRDLLGQEE				

<i>mPatched2</i>	QAFTHCEASSQHVVITILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEE				
	610	620	630	640	650
<i>hPtch-2</i>	660	670	680	690	700
	ETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLS				
	* ** *				
<i>mPatched2</i>	GTGPQAACRPLLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLS				
	660	670	680	690	700

FIG. 8B

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	710	720	730	740	750
<i>hPtc-2</i>	LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA				

<i>mPatched2</i>	LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA				
	710	720	730	740	750

	760	770	780	790	800
<i>hPtc-2</i>	HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDW				

<i>mPatched2</i>	HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRSWLQGIQAAFDQDW				
	760	770	780	790	800

	810	820	830	840	850
<i>hPtc-2</i>	ASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLV DREGL				

<i>mPatched2</i>	ASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLTTRKLV DKEGL				
	810	820	830	840	850

	860	870	880	890	900
<i>hPtc-2</i>	IPPELFYMG LTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP				

<i>mPatched2</i>	IPPELFYMG LTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP				
	860	870	880	890	900

	910	920	930	940	950
<i>hPtc-2</i>	PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP				

<i>mPatched2</i>	AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSP				
	910	920	930	940	950

	960	970	980	990	1000
<i>hPtc-2</i>	FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMT				

<i>mPatched2</i>	FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMT				
	960	970	980	990	1000

	1010	1020	1030	1040	1050
<i>hPtc-2</i>	VELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLT TQGSRNLR				

<i>mPatched2</i>	VELFGIMGFLGIKLSAIPVVILVASIGIGVEFTVHVALGFLT SHGSRNLR				
	1010	1020	1030	1040	1050

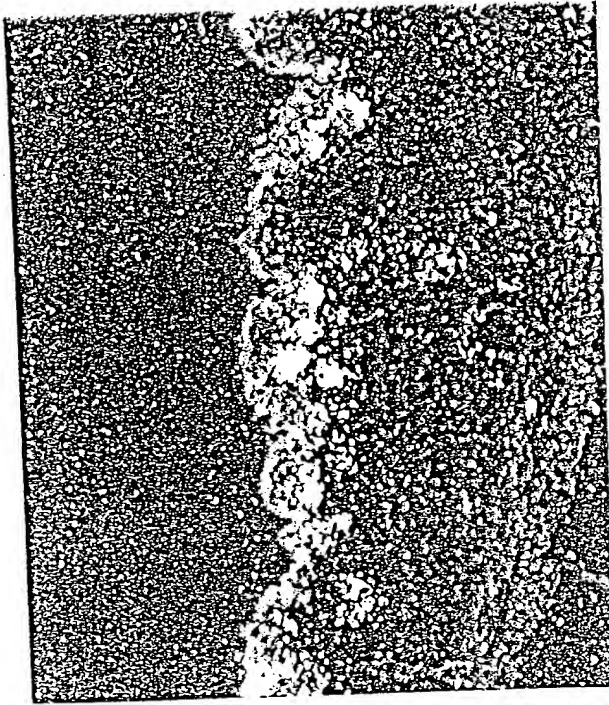
FIG. 8C

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	1060	1070	1080	1090	1100
<i>hPtch-2</i>	AAHALEHTFAPVTDGAISTLLGLMLAGSHFDFIVRYFFAALTVLTLGL				
	** ***.*****.*****.*****.*****.*****				
<i>mPatched2</i>	AASALEQTFAPVTDGAVSTLLGLMLAGSNFDFIIRYFFVVLTVLTLGL				
	1060	1070	1080	1090	1100
	1110	1120	1130	1140	1150
<i>hPtch-2</i>	LHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGASSSLP				
	****.*****.***.*****.***.*****.*****				
<i>mPatched2</i>	LHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGGLRWDRPPTLP				
	1110	1120	1130	1140	1150
	1160	1170	1180	1190	1200
<i>hPtch-2</i>	QSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP				
	*****.*****.***.***				
<i>mPatched2</i>	QSFARVTTSMTVLHPPPLPGAYVHPASEEPT				
	1160	1170	1180		
<i>hPtch-2</i>	ATG				

FIG. 8D

PTCH2



PTCH



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FIG. 9

~~Consensus sequence of human patched 2 cDNA clone~~
~~length: 4004 bp~~

~~SEQ ID NO: 8~~

1 CCCACGGTC CGGGAGAAGC TGGGGAGGA GGCTGCATAC ACCTCTCAGA TGCTGATACA GACCGCACGC CAGAGGGAG AGAACATCTT CACACCCGAA
GGGTGGCGAG GCCCTCTTCG ACCCCCTCTT CGACGATATG TGGAGAGTCT ACGACTATGT CTGGCGTGGG GTCCTCCCTC TCTGTAGGA GTGTGGGCTT

101 GCACTTGGCC TCCACCTCGA GGCAGCCCTC ACTGCCAGTA AAGTCCAAGT ATCACTCTAT GGGAAAGTCT GGGATTGAA CAAATCTGC TACAAGTCAG
CGTGAACCG AGGTGGAGGT CCGTCGGGAG TGACGGTCTAT TTCAGGTTCA TAGTGAGATA CCTTTCAGGA CCTTAAACTT GTTTAGACG ATGTTCAETC

201 GAGTTCCCTT TATTGAAAT GGAATGATTG AGCGGATCAT TGAGAAAGCTG TTTCCGTGGG TGATCCTCAC CCCCCTCGAC TGCTTCTGGG AGGAGCCAA
CTCAAGGGA ATAACTTTTA CCTTACTAAC TCGCCTACTA ACTCTTCGAC AAAGGCACGC ACTAGGAGTG GGGGAGCTG ACGAAGACCC TCCCTCGGTT

301 ACTCAAGGG GGTCCGCTT ACCTGCCGCT CCCAATGTGG CTCACAGCT GAGTGGGGG TGCCATGGCT TCTCCACAA ATTTCATGCAC TGGCAGGAGG
TGAGGTTCCC CCGAGGCGGA TGGACGGCGA GGGTTACACC GAETGCTCGA CTCACCCCG ACGGTACCGA AGAGGTGT TAAGTACGTG ACCGTCTCC

401 AATTGCTGCT GGGAGGCATG GCCAGAGACC CCCAAGGAGA GCTGCTGAGG GCAGAGGCCG CACAGTGTCTG ATGAGTCCCC GCCAGCTGTA
TTAACGACGA CCTCCCGTAC CGGTCTCTGG GGGTTCTCT ACTGTAAACG ACCTCACTCC CGTCTCCGGG ACGTCTCGTG GAAGAACGAC TACTCAGGGG CGGTCTGACAT

501 CGAGCATTTT CCGGGTGACT ATCAGACACA TGACATTGGC TGGAGTGAGG AGCAGGCCAG CACAGTGTCTA CAAGCCTGGC AGCGGCGCTT TGTGCAGGTC
GCTCGTAAAG GCCCCACTGA TAGTCTGTGT ACTGTAAACG ACCTCACTCC TCGTCCGGTC GTGTACGAT GTTCGGACCG TCGCCGCGAA ACAGTCCAG

601 GGTATGGACA AGGACAGGGG GGTGCCCTGA GGCAATTCCC TCCTCCTGCC CCTCCTATC CACCTGTCTT CTCAGCTGG CCCAGGAGGC CCTGCCCTGAG
CCATACCTGT TCCTGTCCCC CCACGGGACT CCGGTAAGGG AGGAGGACCG GGGAGGATAG GTGGGACAAA GAGTCTGACC GGTCTCTCCG GGACGGGACTC

701 AACGCTTCCC AGCAGATCCA TGCCCTTCTCC TCCACACACC TGGATGACAT CCTGCATGGG TTCTCTGAAG TCAGTGTCTGC CCGTGTGGTG GGAGGCTATC
TTGCGAAGGG TCGTCTAGGT ACGGAGAGG AGGTGGTGGG ACCTACTGTA GGACGTACCC AAGAGACTTC AGTCAGGACG GGCACACCCAC CCTCCGATAG

801 TGCTCATGGT GGGTCTTGCA CCTGGCACCT TGCCCCCACC CCACCTCCAA CCAGTGCCCA CCTTGGGAG CCCCCTTGAC TGCCCTTTCC CCCCACAGCT
ACGAGTACCA CCCAGAACCT GGACCGTGGA ACGGGGGTGG GGTGAGGTT GTTCACGGGT GGGACCCCTC GGGGAAAGG GGGGTGTGGA

FIG. 10A

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901 GGCCTATGCC TGTGTGACCA TGCTGCGGTG GGACTGGCC CAGTCCGAGG GTTCCGTGGG CTTTGCCGGG GTACTGCTGG TGGCCCTGGC GGTGGCCTCA
CCGATACCG ACACACTGGT ACGACGCCAC CCTGACGCGG GTCAGGGTCC CAAGGCACCC GGAACGGCCC CATGACGACC ACCGGGACCG CCACCGGAGT

1001 GGCCTTGGGC TCTGTGCCCT GCTCGGCATC ACCTTCAATG CTGCCACTAC CCAGGTACGC CAGGACTGCA GGGCAGACTC AGTGCCAGTC ACCAGGCTTC
CCGAACCCG AGACACGGGA CGAGCCGTAG TGAAGTTAC GACGGTATG GGTCCATGCG GTCTGTGACG CCGTCTGAG TCACGGTCAG TGGTCCGAAG

1101 ACGGGTCTC AGTGCCCCG TCTCTGCCC CTCCAGGTGC TGCCCTTCTT GACTCTGGGA ATCGCGTGG ATGACGTATT CCTGTGGCG CATGCCCTCA
TGCCAGGAG TCGACGGCG AGGACACGGG GAGTCCACG ACGGGAAGAA CTGAGACCTT TAGCCGACC TACTGCATAA GGACGACCGC GTACGGAAGT

1201 CAGAGGCTCT GCCTGGCACC CCTCTCCAGG TGGGGCCTTG TCCCCCAGG CTCACTGAG GCAGCTCAGC TTAAGTTA AGAGCTCTT GGTCAAGTG
GTCTCCGAGA CGGACCGTGG GGAGAGGTCC ACCCCGGAAC AGGGGTCCC GAGTAGACTC CGTCGAGTCG AATGACCAAT TCTCGGAGAA CCAAGTTCAC

1301 ACCTTGGCT GCTAATGAC CTGGGTGCTT CTTGTCCCCA TGTGTAAACA GGGAAATAA TAGTGTGTG TCTAAGGGT TATTGTTGG ATCAGTGAAG
TGGAAACCGA CGATTACTG GAGCCACGGA GAACAGGGGT ACACATTGT CCCCTTATT ATCAGGACAC AGGATTCCCA ATAACAAACC TAGTCACTTC

1401 TAACTCAAGT TGAATGCTTA GAACAGCCCC TCATAGTAC ATGTACCCA ATAAATGCTA GCCACTGTGT TATGACTGCC CCACCTCTGC ACCCAAGTT
ATTGAGTTCA ACTTACGAAT CTTGTCCGGT AGTATGCATG TACCATTGGT TATTACGAT CCGTGACACA ATACTGACGG GTTGAGACG TGGGGTTCAA

1501 CCTCAGCCTC CCTTCACTC CACTTTGACA CGGCCCTCC CTTGTACCT GAGGCGAGT CCCCACCTG TCCTGGCAGG AGGCATGGG CGAGTGTCTG
GGACTCGGAG GGAAGTGAG GTGAACTGT GCCGGGAGG GAACACTGGA CTCCGCTCA GGGGTGAGAC AGGACCTCC TCGGTACCC GTCACAGAC

1601 CAGCGCACGG GCACCAAGTGT TGTACTACA TCCATCAACA ACATGGCCG CTTCTCTCATG GCTGCCCTCG TTCCCATCCC TGGGTGCGA GCCTTCTCCC
GTCCGCTGCC CGTGGTCACA ACATGAGTGT AGGTAGTTGT TGTACCGCG TGTACCGGAGTAC CGACGGGAGC AAGGTAGGG ACGCAGCGT CGGAAGAGGG

1701 TACAGCCTGG ACCTACGGCG GCGCCACTGC CAGCGCCTTG ATGTGCTCG CTGCTTCTCC AGGTACTGCC TGGCCCCCAG CCCCTTCTC CCGTGACCCA
ATGTCGACC TGGATGCCG CGCGGTGACG GTCGCGGAAC TACACGAGAC GACGAAGAGG TCCATGACGG ACGCGGGTC GGGGAAGGAG GGCATGGGT

1801 CGCCAGCCTG TCCCCTCAC AGCATTTCAA GGCACAGACC TGTATCCAC TCTCTACCTC TTCCAGTCCC TGCTCTGCTC AGGTGATTCA GATCCTGCCC
GCGTCCGAC AGGGAGTGG TCGTAAAGTT CCGTGTCTGG ACAGTAGGTG AGAGTGGAG AAGTCAAGG AAGTCAAGG TCCACTAAGT CTAGACGGG

1901 CAGGAGCTGG GGGACGGAC AGTACCAGTG GGCATTGCC ACCTCACTGC CACAGTTCAA GCCTTTACCC ACTGTGAAGC CAGCAGCCAG CATGTGGTCA
GTCCCTCGACC CCTGCCCCTG TCATGGTCA CCGTAACGGG TGGAGTGAC GTGTCAAGTT CGGAATGGG TGACACTTCG GTCGTCCGTC GTACACAGT

2001 CCATCCTGCC TCCCCAAGCC CACCTGGTGC CCCACCTTC TGACCCACTG GGCTCTGAGC TCTTCAGCCC TGGAGGTCC ACACGGGACC TTCTAGGCCA
GGTAGGACG AGGGTTCCG GTGGACCACG GGGGTGGAAG ACTGGGTGAC CCGAGACTCG AGAGTCCGG ACCTCCCAGG TGTGCCCTGG AAGATCCGGT

FIG. 10B

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2101 GGAGGAGAG ACAAGGCAGA AGGAGCCTG CAAGTCCCTG CCCTGTGCCC GCTGAATCT TGCCATTTC GCGCGTATC AGTTGCCCC GTTGCTGCTC
 CCTCTCCTC TGTTCCTCT TCCGTGGAC GTTCAGGGAC GGGACACGG CGACCTTAGA ACGGATAAG CCGGCGATAG TCAACGGGG CAACGACGAG

2201 CAGTCACATG CCAGGCCAT CGTGCTGGT CTCTTTGGT CTCTTCTGG CCTGAGCCTC TAGGAGCCA CTTGGTGCA AGACGGCCTG GCCCTGACGG
 GTCAGTGAC GTTCCGTA GCAGACACG GAGAACCAC GAGAAGACC GAGTCCGAG ATGCTCGGT GGAACACGT TCTGCCGGAC CGGACTGCC

2301 ATGTGGTGC TCGGGGCACC AAGGAGCATG CCTTCCTGAG CGCCAGCTC AGGTACTTCT CCCTGTACGA GTTGGCCCTG GTGACCCAGG GTGGCTTTGA
 TACACCACG AGCCCGTGG TTCTCTGTAC GGAAGACTC GCGGTCTGAG TCCATGAAGA GGGACATGCT CCACCGGAC CACTGGGTCC CACCGAACT

2401 CTACGCCCC TCCCAACGG CCTCTTTGA TCTGCACCAG CGCTTCAGT CCCTCAAGC GTGTGCTGCC CCACCGGCCA CCCAGGCACC CCGCACCTGG
 GATCGGGTG AGGTTGGC GGGAGAACT AGACGTGGT GCGAAGTCAA GGGAGTCCG CCACGACGG GGTGCCCGT GGTCCGTGG GCGTGGACC

2501 CTGCACTATT ACCGCAACTG GCTACAGGA ATCCAGGCTG CCTTTGACCA GGAAGTGGT TCTGGGCGCA TCACCGGCCA CTGTAACCG AATGGCTCTG
 GACGTGATAA TGGCTTGAC CGATGTCCT TAGGTCCGAC GGAAGTGGT CTGACCCGA AGACCCCGT AGTGGCGGT GAGCATGGC TTACCGAGAC

2601 AGGATGGGC CTGGCCTAC AAGCTGCTCA TCCAGACTGG AGAGCCCGC GAGCCTCTG ATTCAGCCA GGTGGGAGA GGGCTGGAGG GTTCCACTAG
 TCCTACCCCG GGACCGATG TTCGACGAGT AGGTCTGACC TCTGCGGTC CTCGGAGACC TAAAGTCCGT CCAACCTCT CCCGACCTCC CCAGGTGATC

2701 TACAGGGGT GAGGCCCTC TGGGCCCAG CCTTCAGCC TCTCTGCTC TGAGCTGAC CACAAGGAG CTGGTGGACA GAGAGGACT GATTCCACCC
 ATGTCCCGA CGTCCGAGG ACCCGGTCC GGAAGTCGG AGAGACGGAG ACGTCGACTG GTGTTCTTC GACCACCTGT CTCTCCCTGA CTAAGGTGG

2801 GAGCTCTTCT ACATGGGGCT GACCGTGTG GTGAGCAGT ACCCCCTGG TCTGGCAGCC TCACAGGCCA ACTTCTACCC CCCACCTCT GAATGGCTGC
 CTCGAGAAGA TGTACCCCGA CTGGCACACC CACTCGTAC CACTCGTAC TGGGGGACCC AGACGTCGG AGTGTCCGT TGAAGATGG GGTGGAGGA CTTACCGACG

2901 ACGACAATA CGACACCACG GGGGAGAACC TTGCGAGTGA GTCTTGGGG GAGCTCGGA AGAGCCTCAG CCTGCGCCAC ACAAGCCTG AGCTGAGGC
 TGCTGTTAT GCTGTGGTG CCTCTTGG AAGCTCACT CAGAACCCCT CTCGAGCCCT TCTCGGATC GGAGCGGTG TGTTCGGAC TCGACTCCG

3001 CCTGCCCACT CTGCCCCGTG CTCACCGCCC TGTCCCTCTC CCTCTTCTC CTTCCTCTC CCGCCAGCT CAGCCCTGG AGTTGCCCA
 GGACGGGTGA GACGGGCAC GAGTGGCGG ACAGGGAGG GGAGGAGG GGAGGTGTCA GGGCGTCA GGGCGTCA GTCCGGAACC TCAACGGGT

FIG. 10C

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3101 GTTCCCTTC CTGCTGCTG GCCTCCAGAA GACTGCAGAC TTTGTGGAGG CCATCGAGGG GGCCCGGGCA GCATGCGCAG AGCCGGGCCA GGCTGGGGTG
CAAGGGGAG GACGACGCAC CGGAGGTCTT CTGAGGTCTG AAACACCTCC GGTAGTCCC CCGGGCCCGT CGTAGCGGTC TCCGGCCGCT CCGACCCACAC

3201 CACGCCCTACC CCAGCGGCTC CCCCTTCCTC TTCTGGGAAC AGTATCTGGG CCTGCGGGCC TGCTTCCTGC TGGCGGCTG CATCCTGCTG GTGTGCACCT
GTGCGGATGG GGTGCGCCAG GGGGAAGGAG AAGACCTTG TCATAGACCC GGACGCGCGG ACGAAGACG ACCGACAGAC GTAGGACGAC CACACGTGAA

3301 TCCTCGTCTG TGCTCTGCTG CTCCTCAACC CCTGGACGGC TGGCCTCATA GTGAGTGCTT GCAGGAGTGG GGACAGAGAC ACCCACCTT TCCCTGCCCA
AGGAGCAGAC ACGAGACGAC GAGGAGTTGG GGACCTGCCG ACCGAGTAT CACTCAGAA CGTCCCTCACC CCTGTCTCTG TGGGGTGGGA AGGACGGGT

3401 GCCTGTATC CCTCCTGCCA GGAGCCCTCT GTGAGCCCTG TCTCCCTCAG GTGCTGGTCC TGGCGATGAT GACAGTGAAC CTCTTTGGTA TCATGGGTTT
CGGACAGTAG GGAGGACGGT CCTCGGGAGA CACTCGGGAC AGAGGAGTC CACGACCGG ACCGCTACTA CTGTACCTT GAGAAACCAT AGTACCCAAA

3501 CCTGGGCATC AAGCTGAGTG CCATCCCGT GGTGATCCTT GTGGCCTCTG TAGGCATTGG CGTTGAGTTC ACAGTCCACG TGGCTCTGGT GAGCACGGGC
GGACCCGTAG TTCGACTCAC GGTAGGGGCA CCACTAGGAA CACCGGAGAC ATCCGTAACC GCAACTCAAG TGTGAGTGC ACCGAGACCA CTCGTGCCCG

3601 ACCCCGGGA GGACCAATC AGCTGATTCA GTATTCAACA CATATTGTTT AAGCCCTAC TATGTGCTAG GTACTATTTA AGAATTTGG CTGGGTGGAC
TGGGGCCCT CCCTGGTTAG TCGACTAAGT CATAAGTTGT GTATAACAAG TTCCGGGATG ATACAGATC CATGATAAAT TCTTAAACCC GACCCACCTG

3701 GTGGTGGCTC ATTCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCGGGTG GATCACCTGA GGTGCGGAGT TCGAAACCAG CCTGGCCCAAC ATGGTGAAAC
CACCACCGAG TAAGGACATT AGGTCTGTGA AACCTCCGG CTCGCGCCAC CTAGTGGACT CCAGCCCTCA AGCTTTGGTC GGACCGGTTG TACCACCTTG

3801 CCTGTCTTTA CTAAAAATAC AAAAAATTAG CCAGGCGTGG TGGCACATGC CAGTAGTCCC AGCTACTTTG GAGGCTGAGG CAGAATTGCT TGAACCTGGG
GGACAGAAAT GATTTTATG TTTTAAATC GGTCCGCACC ACCGTGTACG GTCATCAGG TCGATGAAAC CTCCGACTCC GTCTTAAACGA ACTTGGACCC

3901 AGGCGAAGGT TGCAGTGAGC CCATTGCCT CCAGCCTGGG CAACAGAGT GCAACTCTCC GTCTCAAAAA AAAAAAAA AAGGCGGGCC
TCCGCTTCCA ACGTCACTCG ACTCTAGCAC GGTAACGTGA GGTGTTCTCA GGTGAGAGG CAGAGTTTTT TTTTTTTTTT TTCCCGCCCG

4001 GCGA
CGCT

FIG. 10D

~~clone 16-1 human patched 2~~
~~length 2082 bp~~

(SEQ ID NO: 9)

1 TTCCGGCATG ACTCGATCGC GCGCCCTCAG AGAGCTGCCC CCGAGTTACA CACCCCCAGC TCGAACCCGA GCACCCGAGA TCCTAGCTGG GAGCTGAAG
AAGGCCGTAC TGAGCTAGCG CCGGGGAGTC TCTCGACGGG GGCTCAATGT GTGGGGTCTG AGCTTGGCGT CGTGGGTCT AGGATCGACC CTCGGACTTC
101 GCTCCACTCT GGCTTCGTGC TTACTTCCAG GGCCTGCTCT TCTCTCTGGG ATGCGGGATC CAGAGACATT GTGGCAAAGT GCTCTTTCTG GGAATGTTGG
CGAGGTGAGA CCGAAGCAG AATGAAGGTC CCGGACGAGA AGAGAGACCC TACCCCTAG GTCTCTGTAA CACCGTTTCA CGAGAAAGAC CTTGACAACC
201 CCTTTGGGC CTTGGCATTG GGTCTCCGA TGGCCATTAT TGAGACAAC TTGGAACAGC TCTGGGTAGA AGTGGGCAGC CGGTGAGCC AGGAGCTGCA
GGAAACCCCG GGACCGTAAT CCAGAGCGGT ACCGGTAATA ACTCTGTTTG AACCTTGTCG AGACCCATCT TCACCCGTCTG GCCCACCTCG TCCCTGACGT
301 TTACACCAAG GAGAAGCTGG GGGAGGAGGC TGCATACACC TCTCAGATCC TGATACAGAC CCGACGCCAG GAGGGAGAGA ACATCCTCAC ACCCGAAGCA
AATGTGGTTC CTCTTCGACC CCTCCTCCG ACGTATGTGG AGAGTCTACG ACTATGTCTG GCGTGGGTCT CTCCCTCTCT TGTAGGAGTG TGGGCTTCGT
401 CTTGGGCTCC ACCTCCAGGC AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAGTCTCTGG ATTTGAACAA AATCTGCTAC AAGTCAGGAG
GAACCGGAGG TGGAGGTCCG TCGGAGTGA CCGTCATTTC AGGTTTCATAG TGAGATACCC TTCAGGACCC TAAACTTGT TTAGACGATG TTCAGTCTCTC
501 TTCCCTTTAT TGAATAATGA ATGATTGAGT GGATGATTGA GAAGCTGTTT CCGTGCTGA TCCTCACCCC CCTCGACTGC TTCTGGGAGG GAGCCAAACT
AAGGGGAATA ACTTTACCT TACTAACTCA CCTACTAACT CTTCGACAAA GGCACGCACT AGGAGTGGGG GGAGCTGACG AAGACCTCC CTCGGTTTGA
601 CCAAGGGGGC TCCGCCCTACC TGCCCGGGCCG CCGGATATC CAGTGGACCA ACCTGGATCC AGAGCAGCTG CTGGAGGAGC TGGTCCCTTT TGCCTCCCTT
GGTTCCCGCG AGCGGATGG ACGGGCCGGC GGGGCTATAG GTCACCTGGT TGGACCTAGG TCTCGTCGAC GACCTCCTCG ACCCAGGGAA ACGGAGGGAA
701 GAGGGCTTCC GGGAGCTGCT AGACAAGGCA CAGGTGGGCC AGGCTTACGT GGGGGGGCC TGTCTGCACC CTGATGACCT CCACTGCCCC CTTAGTGCCC
CTCCCGAAGG CCCTCGACGA TCTGTTCCGT GTCCACCCCG TCCGGATGCA CCGCGCCGG ACAGACGTGG GACTACTGGA GGTGACGGGT GGATCACGGG
801 CCAACCATCA CAGCAGCAG GCTCCCAATG TGGCTCACGA GCTGAGTGG GGCTGCCCCA CAATTCATG CACTGGCAGG AGGAATTGCT
GGTTGGTAGT GTGTCCTCTC CGAGGGTTAC ACCGAGTGCT CGACTCACCC CCGACGGTAC CGAAGAGGT GTTTAAGTAC GTGACCGTCC TCCTTAACGA
901 GCTGGGAGGC ATGGCCAGAG ACCCCCAAGG AGAGTCTGCT AGGGCAGAG CCCTGCACAG CACCTTCTTG CTGATGAGTC CCGCCAGCT GTACGAGCAT
CGACCTCCG TACCGGTCTC TGGGGTTCC TCTCGACGAC TCCCGTCTCC GGGACGTCTC GTGGAAGAAC GACTACTCAG GGGCGGTCTG CATGCTCGTA

FIG. 11A

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1001 TTCCGGGGTG ACTATACAGAC ACATGACATT GGCTGGAGTG AGGACAGGC CAGCACAGTG CTACAAGCCT GGCAGCGGCG CTTTGTGTCAG CTGGCCCCAGG
AAGCCCCCAC TGATAGTCTG TGTACTGTAA CCGACCTCAC TCCTCGTCCG GTCGTGTAC GATGTTCCGA CCGTCGCGC GAAACACGTC GACCGGGTCC

1101 AGGCCCTGCC TGAGAACGCT TCCCACAGAG TCCATGCCTT CTCCTCCACC ACCTGGATA ACATCCTGCA TCGGTTCTCT GAAGTCAGTG CTGCCCGTGT
TCCGGGACGG ACTCTTGCA AGGTCTCT AGGTACGGAA GAGGAGGTGG TGGACCTAT TGTAGGACGT ACGCAAGAGA CTTCACTAC GACGGGCACA

1201 GGTGGGAGGC TATCTGTCTA TGCTGGCCTA TGCCTGTGTG ACCATGCTGC GGTGGACTG CGCCCAGTCC CAGGGTTCCG TGGGCTTGC CGGGTACTG
CCACCCTCCG ATAGACGAGT ACGACCGGAT ACGACAGAC ACGGACAGAC TGGTACGACG CCACCCTGAC GCGGTCAAG GTCCCAAGC ACCCGAAGC GCCCATGAC

1301 CTGGTGGCCC TGGCGGTGGC CTCAGGCCTT GGGCTCTGTG CCTGCTCGG CATCACCTTC AATGCTCCA CTACCCAGGT GTCGCCCTTC TTGGCTCTGG
GACCACGGG ACCGCCACCG GAGTCCGAA CCGAGACAC GGGACGAGC GTAGTGAAG TTACGACGGT GATGGTCCA CGACGGGAAG AACCGAGACC

1401 GAATCGGCGT GGATGACGTA TTCCTGTGTG CGCATGCTT CACAGAGGCT CTGCTCGGCA CCCCTCTCCA GGAGCGCATG GGGAGTGTG TGCAGCGCAC
CTTAGCCGCA CCTACTGCAT AAGGACGACC GCGTACGGAA GTGTCTCCGA GACGACCGT GGGGAGAGT CCTCGGTAC CCGTCAACAG ACGTCGCGTG

1501 GGGACACCAGT GTCGTACTCA CATCCATCAA CAACATGSCC GCCTTCTCTA TGCTGCTCTA GGTGCTGC CCGTCCCTTC CTTACAGCCA
CCCGTGGTCA CAGCATGAGT GTAGTAGT GTTGTACCG GTTGTACCGA CCGAAGGAGT ACCGACGAGT CCAAGGCTAG GGACGGGACG CTCGGAAGAG GAATGTCGGT

1601 TCCTCAGCCT GGACCTACGG CCGCGCCACT GCCAGCGCCT TGATGTGCTC TGCTGCTTCT CCAGTCCCTG CTCTGCTCAG GTGATTGAGA TCCTGCCCCA
AGGAGTCGGA CTGGATGCC CCGCGGTGA CCGTCCGGA ACTACACGAG ACGACGAAGA GGTCAAGGAC GAGACGAGTC CACTAAGTCT AGGACGGGGT

1701 GGAGCTGGGG GACGGGACAG TACCAGTGGG CATTGCCCCAC CTCACTGCCA CAGTTCAAAG CTTTACCCAC TGTGAAGCCA GCAGCCAGCA TGTGGTCACC
CCTCGACCCC CTGCCCTGTC ATGGTCACCC GTAACGGGTG GAGTGACGGT GTCAGATTCTG GAAATGGGTG ACATTTCGGT CGTCGGTCTG ACACCAAGTG

1801 ATCCTGCTC CCCAAGCCCCA CCTGGTGCC CCTGCTCTG ACCACTGGG CTCTGAGCTC TTCAGCCCTG GAGGTGCCAC ACGGACCTT CTAGGCCAGG
TAGGACGGAG GGGTTCGGGT GAACACGGG GGTGGAAGAC TGGGTGACCC GAGACTCGAG AAGTCGGGAC CTCCCAGGTG TGCCCTGGAA GATCCGGTCC

1901 AGGAGGAGAC AAGGCAGAAG GCAGCCTGCA AGTCCCTGCC CTGTGCCCGC TGGAACTTG CCCGGAATTC CTGCAGCCCC GGGGATCCAC
TCCTCCTCTG TTCCGTCTTC CGTCGGACGT TCAGGGACGG GACACGGGCG ACCTTAGAAC GGGTAAAGCG GGGCCTTAAG GACGTCGGGC CCCCTAGGTG

2001 TAGTTCTAGA GCGGCGGCCA CCGCGGTGGA GCTCCAGCTT TTGTTCCCTT TAGTGAGGGT TAATTGCGCG CTTGGGTATC TT
ATCAAGATCT CGCCGGCGGT GGCCCCACCT CGAGTCTGAA AACAAAGGAA ATCACTCCCA ATTAACGCGC GAACCCATAG AA

FIG. 11B

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